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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/531,438A

DATE: 08/22/2002

TIME: 16:47:46

Input Set : A:\EP.txt

Output Set: N:\CRF3\08222002\I531438A.raw

ENTERED

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3 <110> APPLICANT: GILBERT, MARYSE
4      POPOFF, MICHEL-ROBERT
6 <120> TITLE OF INVENTION: CLOSTRIDIUM TOXIN, AND PROCESS FOR THE PREPARATION OF
IMMUNOGENIC
7      COMPOSITIONS
9 <130> FILE REFERENCE: 0660-0172-0CONT
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/531,438A
12 <141> CURRENT FILING DATE: 2000-03-20
14 <150> PRIOR APPLICATION NUMBER: PCT/FR98/01999
15 <151> PRIOR FILING DATE: 1998-09-17
17 <150> PRIOR APPLICATION NUMBER: FR971170
18 <151> PRIOR FILING DATE: 1997-09-19
20 <160> NUMBER OF SEQ ID NOS: 7
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1392
26 <212> TYPE: DNA
27 <213> ORGANISM: Clostridium perfringens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (268)..(1065)
32 <223> OTHER INFORMATION:
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37 gatataattaa ttatatagct gaaaatttat aattatatga taagtatagt taataaataa      120
39 aaagtgttct cgggggacac ttttttgttt taaaaaggaa aatataaata aaatttagat      180
41 aaaagtgtaa aataattatt tttattttaa atttggttaa aatttgatat aattgaattg      240
43 taaaaaaaaat ttcagggggg aatataa atg aaa aaa att att tca aag ttt act      294
44                                     Met Lys Lys Ile Ile Ser Lys Phe Thr
45                                     1           5
47 gta att ttt atg ttt tca tgt ttt ctt att gtt gga gca ata agt cca      342
48 Val Ile Phe Met Phe Ser Cys Phe Leu Ile Val Gly Ala Ile Ser Pro
49 10           15           20           25
51 atg aaa gca agt gca aaa gaa atc gac gct tat aga aag gta atg gag      390
52 Met Lys Ala Ser Ala Lys Glu Ile Asp Ala Tyr Arg Lys Val Met Glu
53           30           35           40
55 aat tat ctt aat gct tta aaa aac tac gat att aat aca gtt gta aac      438
56 Asn Tyr Leu Asn Ala Leu Lys Asn Tyr Asp Ile Asn Thr Val Val Asn
57           45           50           55
59 att tca gaa gat gaa aga gta aat aat gtt gaa cag tat aga gaa atg      486
60 Ile Ser Glu Asp Glu Arg Val Asn Asn Val Glu Gln Tyr Arg Glu Met
61           60           65           70
63 tta gaa gat ttt aaa tat gat cct aac caa caa ctg aaa tct ttt gaa      534
64 Leu Glu Asp Phe Lys Tyr Asp Pro Asn Gln Gln Leu Lys Ser Phe Glu

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65      75      80      85
67 ata ctt aat tca caa aag agc gat aat aaa gaa ata ttt aat gta aaa      582
68 ile leu asn ser gln lys ser asp asn lys glu ile phe asn val lys
69 90      95      100      105
71 act gaa ttt tta aat ggt gca att tat gat atg gaa ttt act gta tca      630
72 thr glu phe leu asn gly ala ile tyr asp met glu phe thr val ser
73      110      115      120
75 tct aaa gat gga aaa tta ata gta tct gat atg gaa aga aca aaa gtt      678
76 ser lys asp gly lys leu ile val ser asp met glu arg thr lys val
77      125      130      135
79 gag aat gaa gga aaa tat att tta aca cca tca ttt aga act caa gtt      726
80 glu asn glu gly lys tyr ile leu thr pro ser phe arg thr gln val
81      140      145      150
83 tgt aca tgg gat gat gaa cta gca caa gca att ggg gga gtt tat cca      774
84 cys thr trp asp asp glu leu ala gln ala ile gly gly val tyr pro
85      155      160      165
87 caa aca tat tct gat aga ttt aca tat tat gca gat aat ata tta tta      822
88 gln thr tyr ser asp arg phe thr tyr tyr ala asp asn ile leu leu
89 170      175      180      185
91 aac ttc aga caa tat gca act tca ggt tca aga gat tta aaa gta gaa      870
92 asn phe arg gln tyr ala thr ser gly ser arg asp leu lys val glu
93      190      195      200
95 tat agt gtt gta gat cat tgg atg tgg aaa gat gat gtt aaa gct tct      918
96 tyr ser val val asp his trp met trp lys asp asp val lys ala ser
97      205      210      215
99 caa atg gta tat ggt caa aat cct gat tct gct aga caa ata aga tta      966
100 gln met val tyr gly gln asn pro asp ser ala arg gln ile arg leu
101      220      225      230
103 tat ata gaa aaa gga caa tct ttc tat aaa tat aga ata aga att aaa      1014
104 tyr ile glu lys gly gln ser phe tyr lys tyr arg ile arg ile lys
105      235      240      245
107 aac ttt aca cct gca tca att aga gta ttt ggt gaa ggg tat tgt gca      1062
108 asn phe thr pro ala ser ile arg val phe gly glu gly tyr cys ala
109 250      255      260      265
111 tag aaaaaaatat gaagtgaatt agtcacttca tttttttttt actattaatt      1115
113 ttattatata aaaacctaac atacatgaaa gtattcttaa tacagttata tcaaaattaa      1175
115 agtaggggaa ataaaataaa aggctaaaaa ctatattaaa aactataaaa attattaaat      1235
117 taggttttaa ggtgttatat ttatttatga ttataggaat aaatatgcca aatggaataa      1295
119 ataaaagtaa tattaataat tggctataaa agtatacatc attgataaaa gaaaaattac      1355
121 cagtaaaat tgagcttaaa aaattaaatg taaattt      1392
124 <210> SEQ ID NO: 2
125 <211> LENGTH: 265
126 <212> TYPE: PRT
127 <213> ORGANISM: Clostridium perfringens
129 <400> SEQUENCE: 2
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132 1      5      10      15
135 Phe Leu Ile Val Gly Ala Ile Ser Pro Met Lys Ala Ser Ala Lys Glu
136      20      25      30

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139 Ile Asp Ala Tyr Arg Lys Val Met Glu Asn Tyr Leu Asn Ala Leu Lys
140           35           40           45
143 Asn Tyr Asp Ile Asn Thr Val Asn Ile Ser Glu Asp Glu Arg Val
144           50           55           60
147 Asn Asn Val Glu Gln Tyr Arg Glu Met Leu Glu Asp Phe Lys Tyr Asp
148 65           70           75           80
151 Pro Asn Gln Gln Leu Lys Ser Phe Glu Ile Leu Asn Ser Gln Lys Ser
152           85           90           95
155 Asp Asn Lys Glu Ile Phe Asn Val Lys Thr Glu Phe Leu Asn Gly Ala
156           100          105          110
159 Ile Tyr Asp Met Glu Phe Thr Val Ser Ser Lys Asp Gly Lys Leu Ile
160           115          120          125
163 Val Ser Asp Met Glu Arg Thr Lys Val Glu Asn Glu Gly Lys Tyr Ile
164           130          135          140
167 Leu Thr Pro Ser Phe Arg Thr Gln Val Cys Thr Trp Asp Asp Glu Leu
168 145           150           155           160
171 Ala Gln Ala Ile Gly Gly Val Tyr Pro Gln Thr Tyr Ser Asp Arg Phe
172           165          170          175
175 Thr Tyr Tyr Ala Asp Asn Ile Leu Leu Asn Phe Arg Gln Tyr Ala Thr
176           180          185          190
179 Ser Gly Ser Arg Asp Leu Lys Val Glu Tyr Ser Val Val Asp His Trp
180           195          200          205
183 Met Trp Lys Asp Asp Val Lys Ala Ser Gln Met Val Tyr Gly Gln Asn
184           210          215          220
187 Pro Asp Ser Ala Arg Gln Ile Arg Leu Tyr Ile Glu Lys Gly Gln Ser
188 225           230          235          240
191 Phe Tyr Lys Tyr Arg Ile Arg Ile Lys Asn Phe Thr Pro Ala Ser Ile
192           245          250          255
195 Arg Val Phe Gly Glu Gly Tyr Cys Ala
196           260          265
199 <210> SEQ ID NO: 3
200 <211> LENGTH: 267
201 <212> TYPE: DNA
202 <213> ORGANISM: Clostridium perfringens
204 <400> SEQUENCE: 3
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207 gatataattaa ttatatagct gaaaatttat aattatatga taagtatagt taataaataa 120
209 aaagtgttct cgggggacac ttttttgttt taaaaaggaa aatataaata aaatttagat 180
211 aaaagtgtaa aataattatt tttattttaa atttgtttaa aatttgatat aattgaattg 240
213 taaaaaaaaa ttcagggggg aatataa 267
216 <210> SEQ ID NO: 4
217 <211> LENGTH: 90
218 <212> TYPE: DNA
219 <213> ORGANISM: Clostridium perfringens
221 <220> FEATURE:
222 <221> NAME/KEY: CDS
223 <222> LOCATION: (1)..(90)
224 <223> OTHER INFORMATION:
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227 atg aaa aaa att att tca aag ttt act gta att ttt atg ttt tca tgt      48
228 Met Lys Lys Ile Ile Ser Lys Phe Thr Val Ile Phe Met Phe Ser Cys
229 1          5          10          15
231 ttt ctt att gtt gga gca ata agt cca atg aaa gca agt gca      90
232 Phe Leu Ile Val Gly Ala Ile Ser Pro Met Lys Ala Ser Ala
233          20          25          30
236 <210> SEQ ID NO: 5
237 <211> LENGTH: 30
238 <212> TYPE: PRT
239 <213> ORGANISM: Clostridium perfringens
241 <400> SEQUENCE: 5
243 Met Lys Lys Ile Ile Ser Lys Phe Thr Val Ile Phe Met Phe Ser Cys
244 1          5          10          15
247 Phe Leu Ile Val Gly Ala Ile Ser Pro Met Lys Ala Ser Ala
248          20          25          30
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252 <211> LENGTH: 30
253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
257 <223> OTHER INFORMATION: synthetic DNA
259 <400> SEQUENCE: 6
260 gaaatgttta caactgtatt aatatcgtag      30
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264 <211> LENGTH: 23
265 <212> TYPE: DNA
266 <213> ORGANISM: Artificial Sequence
268 <220> FEATURE:
269 <223> OTHER INFORMATION: synthetic DNA
271 <400> SEQUENCE: 7
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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number